Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of the claims in the application:

Listing of Claims:

22. (Canceled)

Claims 25 - 30 (Canceled)

Claims 32 - 46 (Canceled)

47. (New) A structured panel consisting of a plurality of biased combinatorial linear peptide libraries, each library comprising a plurality of different peptides, all peptides of said panel being of the same length, there being one and only one amino acid in a fixed position in said peptides which is both (1) for each library, the same amino acid (a "constant" amino acid) in all peptides of that library, and (b) not the same amino acid in all libraries of said panel, said position being fixed for all peptides in all libraries of said panel, wherein said fixed position is (a) at least five residues from both ends of the peptides or (b) in the middle 50% of the peptides, shown by the formula

$$(Xaa)_m\text{-}R1\text{-}(Xaa)_n$$

wherein R1 is the amino acid at said fixed position, and m and n do not differ by more than two,

wherein each library is a separate and physically distinct entity from all other libraries of the panel, and

wherein the peptides are displayed on viruses.

48. (New) The panel of claim 47 where m and n are each chosen from a range of 2 to 20.

49. (New) The panel of claim 47 wherein m and n are each chosen from a range of 4 to 9.

50. (New) The panel of claim 47 in which the peptides are displayed on cells.

51. (New) The panel of claim 47 wherein the overall diversity of the panel at the fixed position of the peptides is the same as the overall diversity of the panel at each of the other positions of the peptides.

52. (New) The panel of claim 47, wherein there is no position which is the same amino acid for all peptides of the panel.

53. (New) The panel of claim 47 wherein said peptides are of the form

$$L_1\text{-}(Xaa)_m\text{-}R1\text{-}(Xaa)_n\text{-}L_2,$$

where L_1 and L_2 are each independently chosen from the group consisting of nothing and a subsequence of one or more amino acids, said subsequence being the same for all peptides of the panel,

wherein R1 is the amino acid at said first position, and m and n are independently chosen from the range of 2 to 20.

54. (New) The panel of claim 53 wherein if L_1 and L_2 is a subsequence of one or more amino acids, the subsequence is not more than three amino acids.

55. (New) The panel of claim 54 in which $L_1$is nothing, SS-, or SR-, and L_2 is nothing or -SR.

56. (New) A structured panel consisting of a plurality of biased combinatorial linear peptide libraries, each library having one and only one constant amino acid residue at a fixed position for all peptides in all libraries of said panel, wherein, said fixed position in each library is (a) at least five residues from both ends of the peptides or (b) within the middle 50% of the peptides,

wherein the amino acid is assigned to said fixed position is not the same in all libraries of said panel,

each library being a separately screenable and physically distinct entity from all other libraries of the panel in which the peptides are displayed on viruses

wherein said peptides are of the form

$$(Xaa)_m\text{-}R1\text{-}(Xaa)_n$$

where R1 is the amino acid at said first fixed position, and m and n do not differ by more than two, and wherein R1 is selected from tryptophan, proline or tyrosine.

57. (New) A structured panel of biased combinatorial linear peptide libraries, each library comprising a plurality of different peptides, all peptides of said panel being the same length, each library having at least two constant residue

positions, one at a first position and the other at a second position,

wherein said first position is fixed for all libraries in the panel, and is assigned the same residue for all peptides in any given library, but libraries of the panel collectively present a plurality of different residues at said first position,

wherein said first position is (a) at least five amino acids from both ends of the peptides, or (b) is in the middle 50% of the peptides,

wherein said panel comprises a plurality of subpanels, each comprising a plurality of libraries, and in each subpanel, the location of said second position is constant, but said location of said second position varies from subpanel to subpanel so the second positions of said subpanels, collectively scan a plurality of residue positions other than said first position,

wherein the second position is assigned the same residue for all peptides in a given library but the libraries of a given subpanel collectively present a plurality of different residues at said second position,

wherein if said libraries comprise more than two constant residue positions, the constant residue positions other than said first and second positions are constant for all peptides in said panel,

wherein one or more of the other positions of said libraries are variable positions, at which a given library exhibits a plurality of different residues as a result of sequence variation from peptide to peptide,

each library being a separate and physically distinct entity from the other libraries of the panel.

58. (New) The panel of claim 57 in which the second positions collectively scan all residue positions which are variable across the panel as a whole except for said first position.

59. (New) A structured panel of biased combinatorial linear peptide libraries, each library comprising a plurality of different peptides, all peptides of said panel being the same length, each library having at least two biased residue positions, one at a first position and another at a second position, the amino acids allowed in each library at said biased positions being only a subset of the set of amino acids allowed at the remaining positions of said library, and also being only a subset of the set of amino acids allowed at that biased position in the panel as a whole,

wherein the first position is fixed for all libraries in the panel,

and said first position is (a) at least five amino acids from both ends of the peptides, or (b) is in the middle 50% of the peptides,

wherein said panel comprises a plurality of subpanels, each comprising a plurality of libraries, and in each subpanel, the location of the second position is constant, but said location of the second position varies from subpanel to subpanel so the second positions of said subpanels collectively scan a plurality of residue positions other than said first position,

wherein if said libraries comprise more than two constant residue positions, the constant residue positions other than said first and second positions are constant for all peptides in said panel,

each library being a separate and physically distinct entity from the other libraries of the panel.

60. (New) The panel of claim 59 in which the second positions collectively scan all residue positions which are variable across the panel as a whole except for said first position.

61. (New) The panel of claim 59 wherein the panel has an overall diversity which is the same at each position of the peptides, and a given library has a diversity at a biased position which does not exceed 3.

62. (New) A structured panel consisting of a plurality of biased combinatorial linear peptide libraries, each library comprising a plurality of different peptides, all peptides of said panel being of the same length, there being in said peptides, either one position which is or two positions which are (1) for each library, the same amino acid (a "constant" amino acid) in that position in all peptides of that library, and (2) not the same amino acid in that position in all libraries of said panel,

at least one of said positions being fixed for all peptides in all libraries of said panel, said fixed position being (a) at least five residues from both ends of the peptides or (b) in the middle 50% of the peptides,

each library being a separate and physically distinct entity from all other libraries of the panel, in which the peptides are displayed on viruses.